SEQUENCE LISTING

<110> Barnett, Susan
Zur Megede, Jan

<120> POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

<130> 1631.002

<140> 09/475,704
<141> 1999-12-30

<150> 60/152,195
<151> 1999-09-01

<160> 30

<170> PatentIn Ver. 2.0

<210> 1
<211> 60
<212> DNA
<213> Human immunodeficiency virus

<400> 1
gacatcaagc agggccccaa ggagcccttc cgcgactacg tggaccgctt cttcaagacc 60

<210> 2
<211> 60
<212> DNA
<213> Human immunodeficiency virus

<400> 2
gacatccgcc agggccccaa ggagcccttc cgcgactacg tggaccgctt cttcaagacc 60

<210> 3
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag of HIV strain AF110965

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atgggcgccc gcgccagcat cctgcgcggc ggcaagctgg acgcctggga gcgcatccgc 60
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ctggagaagt tcgccctgaa ccccggcctg ctggagacca gcgagggctg caagcagatc 180
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gccttcagcc ccgaggtgat ccccatgttc accgccctga gcgagggcgc cacccccag 540
gacctgaaca cgatgttgaa caccgtgggc ggccaccagg ccgccatgca gatgctgaag 600

gacaccatca acgaggaggc cgccgagtgg gaccgcgtgc accccgtgca cgccggcccc 660
atcgcccccg gccagatgcg cgagccccgc ggcagcgaca tcgccggcac caccagcacc 720
ctgcaggagc agatcgcctg gatgaccagc aacccccccа tccccgtggg cgacatctac 780
aagcggtgga tcatcctggg cctgaacaag atcgtgcgga tgtacagccc cgtgagcatc 840
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ttcgaggaga ccaccccccgg ccagaagcag gagagcaagg accgcgagac cctgaccagc 1440
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<210> 4
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
of HIV strain AF110967

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ctgcgccccg gcggcaagaa gcactacatg ctgaagcacc tggtgtgggc cagccgcgag 120
ctggagggct tcgccctgaa ccccggcctg ctggagaccg ccgagggctg caagcagatc 180
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gccgacggca aggtgagcca gaactacccc atcgtgcaga acctgcaggg ccagatggtg 420
caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
ttcagccccg aggtgatccc catgttcacc gccctgagcg agggcgccac cccccaggac 540
ctgaacacga tgttgaacac cgtgggcggc caccaggccg ccatgcagat gctgaaggac 600
accatcaacg aggaggccgc cgagtgggac cgcctgcacc ccgtgcaggc cggccccgtg 660
gccccccggcc agatgcgcga cccccgcggc agcgacatcg ccggcgccac cagcaccctg 720
caggagcaga tcgcctggat gaccagcaac ccccccgtgc ccgtgggcga catctacaag 780
cggtggatca tcctgggcct gaacaagatc gtgcggatgt acagccccgt gagcatcctg 840
gacatccgcc agggccccaa ggagcccttc cgcgactacg tggaccgctt cttcaagacc 900
ctgcgcgccg agcaggccac ccaggacgtg aagaactgga tgaccgagac cctgctggtg 960
cagaacgcca accccgactg caagaccatc ctgcgcgctc tcggccccgg cgccaccctg 1020
gaggagatga tgaccgcctg ccagggcgtg ggcggccccg gccacaaggc ccgcgtgctg 1080
gccgaggcga tgagccaggc caacagcgtg aacatcatga tgcagaagag caacttcaag 1140
ggcccccggc gcaacgtcaa gtgcttcaac tgcggcaagg agggccacat cgccaagaac 1200
tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
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cccggcaact tcctgcagaa ccgcagcgag cccgccgccc ccaccgtgcc caccgccccc 1380
cccgccgaga gcttccgctt cgaggagacc acccccgccc ccaagcagga gcccaaggac 1440
cgcgagccct accgcgagcc cctgaccgcc ctgcgcagcc tgttcggcag cggccccctg 1500
agccagtaa 1509

<210> 5
<211> 141
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Env common
region of HIV strain AF110968

<400> 5
accatcacca tcacctgccg catcaagcag atcatcaaca tgtggcagaa ggtgggccgc 60
gccatgtacg ccccccccat cgccggcaac ctgacctgcg agagcaacat caccggcctg 120
ctgctgaccc gcgacggcgg c 141

<210> 6
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
gp120 coding region of HIV strain AF110968

<400> 6
agcgtggtgg gcaacctgtg ggtgaccgtg tactacggcg tgcccgtgtg gaaggaggcc 60
aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgaccccctc gtgcgtgacc 300
ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
gagtaccgcc tgatcaactg caacaccagc gccatcaccc aggcctgccc caaggtgagc 540
ttcgacccca tccccatcca ctactgcacc cccgccggct acgccatcct gaagtgcaac 600
aaccagacct tcaacggcac cggcccctgc aacaacgtga gcagcgtgca gtgcgcccac 660
ggcatcaagc ccgtggtgag cacccagctg ctgctgaacg gcagcctggc caagggcgag 720
atcatcatcc gcagcgagaa cctggccaac aacgccaaga tcatcatcgt gcagctgaac 780
aagcccgtga agatcgtgtg cgtgcgcccc aacaacaaca cccgcaagag cgtgcgcatc 840
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tgcatcatca acaagaccga gtggaacagc accctgcagg gcgtgagcaa gaagctggag 960
gagcacttca gcaagaaggc catcaagttc gagcccagca gcggcggcga cctggagatc 1020
accacccaca gcttcaactg ccgcggcgag ttcttctact gcgacaccag ccagctgttc 1080
aacagcacct acagccccag cttcaacggc accgagaaca agctgaacgg caccatcacc 1140
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gccccccca tcgccggcaa cctgacctgc gagagcaaca tcaccggcct gctgctgacc 1260
cgcgacggcg gcaagaccgg ccccaacgac accgagatct tccgccccgg cggcggcgac 1320
atgcgcgaca actggcgcaa cgagctgtac aagtacaagg tggtggagat caagcccctg 1380
ggcgtggccc ccaccgaggc caagcgccgc gtggtggagc gcgagaagcg c 1431

<210> 7
<211> 1944
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
gp140 coding region of HIV strain AF110968

<400> 7
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aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
gagtaccgcc tgatcaactg caacaccagc gccatcaccc aggcctgccc caaggtgagc 540
ttcgacccca tccccatcca ctactgcacc cccgccggct acgccatcct gaagtgcaac 600
aaccagacct tcaacggcac cggcccctgc aacaacgtga gcagcgtgca gtgcgcccac 660
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atcaccctga ccgtgcaggc ccgcctgctg ctgagcggca tcgtgcagca gcagaacaac 1560
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atcaacaact acaccgacac catctaccgc ctgctggagg agagccagaa ccagcaggag 1860
aagaacgaga aggacctgct ggccctggac agctggcaga acctgtggaa ctggttcagc 1920
atcaccaact ggctgtggta catc 1944

<210> 8
<211> 2466
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
gp160 coding region of HIV strain AF110968

<400> 8
agcgtggtgg gcaacctgtg ggtgaccgtg tactacggcg tgcccgtgtg gaaggaggcc 60
aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgacccccct gtgcgtgacc 300

ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
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ttcgacccca tccccatcca ctactgcacc cccgccggct acgccatcct gaagtgcaac 600
aaccagacct tcaacggcac cggcccctgc aacaacgtga gcagcgtgca gtgcgcccac 660
ggcatcaagc ccgtggtgag cacccagctg ctgctgaacg gcagcctggc caagggcgag 720
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aagcccgtga agatcgtgtg cgtgcgcccc aacaacaaca cccgcaagag cgtgcgcatc 840
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ctgcag 2466

<210> 9
<211> 2547
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
signal sequence and gp160 coding region of HIV
strain AF110968

<400> 9
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ttctggatgc tgatcatcag cagcgtggtg ggcaacctgt gggtgaccgt gtactacggc 120
gtgcccgtgt ggaaggaggc caagaccacc ctgttctgca ccagcgacgc caaggcctac 180
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gaccagatgc acgaggacat catcagcctg tgggaccaga gcctgaagcc ctgcgtgaag 360
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agcatgatcg acaacagcaa caagggcgag atgaagaact gcagcttcaa cgtgaccacc 480
gagctgcgcg accgcaagca ggaggtgcac gccctgttct accgcctgga cgtggtgccc 540
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taccaccgcc tgcgcgactt catcctgatc gccgcccgcg tgctggagct gctgggccag 2340
cgcggctggg aggccctgaa gtacctgggc agcctggtgc agtactgggg cctggagctg 2400
aagaagagcg ccatcagcct gctggacacc atcgccatcg ccgtggccga gggcaccgac 2460
cgcatcatcg agttcatcca gcgcatctgc cgcgccatcc gcaacatccc ccgccgcatc 2520
cgccagggct tcgaggccgc cctgcag 2547

<210> 10
<211> 1035
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic a
gp41 coding region of HIV strain AF110968

<400> 10
gccgtgggca tcggcgccgt gttcctgggc ttcctgggcg ccgccggcag caccatgggc 60
gccgccagca tcaccctgac cgtgcaggcc cgcctgctgc tgagcggcat cgtgcagcag 120
cagaacaacc tgctgcgcgc catcgaggcc cagcagcacc tgctgcagct gaccgtgtgg 180
ggcatcaagc agctgcagac ccgcatcctg gccgtggagc gctacctgaa ggaccagcag 240
ctgctgggca tctggggctg cagcggcaag ctgatctgca ccaccgccgt gccctggaac 300

agcagctgga gcaaccgcag ccacgacgag atctgggaca acatgacctg gatgcagtgg 360
gaccgcgaga tcaacaacta caccgacacc atctaccgcc tgctggagga gagccagaac 420
cagcaggaga agaacgagaa ggacctgctg gccctggaca gctggcagaa cctgtggaac 480
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atcagcctgc tggacaccat cgccatcgcc gtggccgagg gcaccgaccg catcatcgag 960
ttcatccagc gcatctgccg cgccatccgc aacatccccc gccgcatccg ccagggcttc 1020

gaggccgccc tgcag 1035

<210> 11
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Env
common region of HIV strain AF110975

<400> 11
agcatcatca ccctgccctg ccgcatcaag cagatcatcg acatgtggca gaaggtgggc 60
cgcgccatct acgccccccc catcgagggc aacatcacct gcagcagcag catcaccggc 120
ctgctgctgg cccgcgacgg cggc 144

<210> 12
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
gp120 coding region of HIV strain AF110975

<400> 12
agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcacccaggc ctgccccaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccca acaacaacac ccgcaagggc 840
atccgcatcg gccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggcccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960

aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
ctggagatca ccacccacag cttcaactgc cgcggcgagt tcttctactg caacaccagc 1080
aagctgttca acagcagcta caacggcacc agctaccgcg gcaccgagag caacagcagc 1140
atcatcaccc tgccctgccg catcaagcag atcatcgaca tgtggcagaa ggtgggccgc 1200
gccatctacg ccccccccat cgagggcaac atcacctgca gcagcagcat caccggcctg 1260
ctgctggccc gcgacggcgg cctggacaac atcaccaccg agatcttccg cccccagggc 1320
ggcgacatga aggacaactg gcgcaacgag ctgtacaagt acaaggtggt ggagatcaag 1380
cccctgggcg tggcccccac cgaggccaag cgccgcgtgg tggagcgcga gaagcgc 1437

<210> 13
<211> 1950
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
gp140 coding region of HIV strain AF110975

<400> 13
agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgaccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcacccaggc ctgccccaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccca acaacaacac ccgcaagggc 840
atccgcatcg gccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggcccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960
aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
ctggagatca ccacccacag cttcaactgc cgcggcgagt tcttctactg caacaccagc 1080
aagctgttca acagcagcta caacggcacc agctaccgcg gcaccgagag caacagcagc 1140
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gccatctacg ccccccccat cgagggcaac atcacctgca gcagcagcat caccggcctg 1260
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ggcgacatga aggacaactg gcgcaacgag ctgtacaagt acaaggtggt ggagatcaag 1380
cccctgggcg tggcccccac cgaggccaag cgccgcgtgg tggagcgcga gaagcgcgcc 1440
gtgggcatcg gcgccgtgat cttcggcttc ctgggcgccg ccggcagcaa catgggcgcc 1500
gccagcatca ccctgaccgc ccaggcccgc cagctgctga gcggcatcgt gcagcagcag 1560
agcaacctgc tgcgcgccat cgaggcccag cagcacatgc tgcagctgac cgtgtggggc 1620
atcaagcagc tgcaggcccg cgtgctggcc atcgagcgct acctgaagga ccagcagctg 1680
ctgggcatct ggggctgcag cggcaagctg atctgcacca ccaccgtgcc ctggaacagc 1740
agctggagca acaagaccca gggcgagatc tgggagaaca tgacctggat gcagtgggac 1800
aaggagatca gcaactacac cggcatcatc taccgcctgc tggaggagag ccagaaccag 1860
caggagcaga acgagaagga cctgctggcc ctggacagcc gcaacaacct gtggagctgg 1920
ttcaacatca gcaactggct gtggtacatc 1950

<210> 14

<211> 2493
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
gp160 coding region of HIV strain AF110975

<400> 14
agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgaccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420

aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcacccaggc ctgccccaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccca acaacaacac ccgcaagggc 840
atccgcatcg gccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggcccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960
aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
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aagctgttca acagcagcta caacggcacc agctaccgcg gcaccgagag caacagcagc 1140
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gccagcatca ccctgaccgc ccaggcccgc cagctgctga gcggcatcgt gcagcagcag 1560
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gagctgaaga agagcgccac cagcctgctg gacagcatcg ccatcgccgt ggccgagggc 2400
accgaccgca tcatcgaggt gatccagcgc atctaccgcg ccttctgcaa catccccccgc 2460
cgcgtgcgcc agggcttcga ggccgccctg cag 2493

<210> 15
<211> 2565

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
signal sequence and gp160 coding region of HIV
strain AF110975

<400> 15
atgcgcgtgc gcggcatcct gcgcagctgg cagcagtggt ggatctgggg catcctgggc 60
ttctggatct gcagcggcct gggcaacctg tgggtgaccg tgtacgacgg cgtgcccgtg 120
tggcgcgagg ccagcaccac cctgttctgc gccagcgacg ccaaggccta cgagaaggag 180
gtgcacaacg tgtgggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagatc 240
gagctggaca acgtgaccga gaacttcaac atgtggaaga acgacatggt ggaccagatg 300
cacgaggaca tcatcagcct gtgggaccag agcctgaagc cccgcgtgaa gctgacccccc 360
ctgtgcgtga ccctgaagtg caccaactac agcaccaact acagcaacac catgaacgcc 420
accagctaca acaacaacac caccgaggag atcaagaact gcaccttcaa catgaccacc 480
gagctgcgcg acaagaagca gcaggtgtac gccctgttct acaagctgga catcgtgccc 540

ctgaacagca acagcagcga gtaccgcctg atcaactgca acaccagcgc catcacccag 600
gcctgcccca aggtgagctt cgaccccatc cccatccact actgcgcccc cgccggctac 660
gccatcctga agtgcaagaa caacaccagc aacggcaccg gcccctgcca gaacgtgagc 720
accgtgcagt gcacccacgg catcaagccc gtggtgagca ccccccctgct gctgaacggc 780
agcctggccg agggcggcga gatcatcatc cgcagcaaga acctgagcaa caacgcctac 840
accatcatcg tgcacctgaa cgacagcgtg gagatcgtgt gcacccgccc caacaacaac 900
acccgcaagg gcatccgcat cggccccggc cagaccttct acgccaccga gaacatcatc 960
ggcgacatcc gccaggccca ctgcaacatc agcgccggcg agtggaacaa ggccgtgcag 1020
cgcgtgagcg ccaagctgcg cgagcacttc cccaacaaga ccatcgagtt ccagcccagc 1080
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tgcaacacca gcaagctgtt caacagcagc tacaacggca ccagctaccg cggcaccgag 1200
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aaggtgggcc gcgccatcta cgccccccccc atcgagggca acatcacctg cagcagcagc 1320
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cgccccccagg gcggcgacat gaaggacaac tggcgcaacg agctgtacaa gtacaaggtg 1440
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gagaagcgcg ccgtgggcat cggcgccgtg atcttcggct tcctgggcgc cgccggcagc 1560
aacatgggcg ccgccagcat caccctgacc gcccaggccc gccagctgct gagcggcatc 1620
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accgtgtggg gcatcaagca gctgcaggcc cgcgtgctgg ccatcgagcg ctacctgaag 1740
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agccagaacc agcaggagca gaacgagaag gacctgctgg ccctggacag ccgcaacaac 1980
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cgcctgggcc gcatcgagga ggagggcggc gagcaggacc gcgaccgcag catccgcctg 2220
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tactggggcc tggagctgaa gaagagcgcc accagcctgc tggacagcat cgccatcgcc 2460
gtggccgagg gcaccgaccg catcatcgag gtgatccagc gcatctaccg cgccttctgc 2520
aacatccccc gccgcgtgcg ccagggcttc gaggccgccc tgcag 2565

<210> 16

<211> 1056
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic a
gp41 coding region of HIV strain AF110975

<400> 16
gccgtgggca tcggcgccgt gatcttcggc ttcctgggcg ccgccggcag caacatgggc 60
gccgccagca tcaccctgac cgcccaggcc cgccagctgc tgagcggcat cgtgcagcag 120
cagagcaacc tgctgcgcgc catcgaggcc cagcagcaca tgctgcagct gaccgtgtgg 180
ggcatcaagc agctgcaggc ccgcgtgctg gccatcgagc gctacctgaa ggaccagcag 240
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agcagctgga gcaacaagac ccagggcgag atctgggaga acatgacctg gatgcagtgg 360
gacaaggaga tcagcaacta caccggcatc atctaccgcc tgctggagga gagccagaac 420
cagcaggagc agaacgagaa ggacctgctg gccctggaca gccgcaacaa cctgtggagc 480
tggttcaaca tcagcaactg gctgtggtac atcaagatct tcatcatgat cgtgggcggc 540
ctgatcggcc tgcgcatcat cttcgccgtg ctgagcatcg tgaaccgcgt gcgccagggc 600
tacagccccc tgagcttcca gaccctgacc cccaacccccc gcggcctgga ccgcctgggc 660

cgcatcgagg aggagggcgg cgagcaggac cgcgaccgca gcatccgcct ggtgcagggc 720
ttcctggccc tggcctggga cgacctgcgc agcctgtgcc tgttcagcta ccaccgcctg 780
cgcgacctga tcctggtgac cgcccgcgtg gtggagctgc tgggccgcag cagcccccgc 840
ggcctgcagc gcggctggga ggccctgaag tacctgggca gcctggtgca gtactggggc 900
ctggagctga agaagagcgc caccagcctg ctggacagca tcgccatcgc cgtggccgag 960
ggcaccgacc gcatcatcga ggtgatccag cgcatctacc gcgccttctg caacatcccc 1020
cgccgcgtgc gccagggctt cgaggccgcc ctgcag 1056

<210> 17
<211> 492
<212> PRT
<213> Human immunodeficiency virus

<400> 17
Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Gly Lys Leu Asp Ala Trp
1 5 10 15

Glu Arg Ile Arg Leu Arg Pro Gly Gly Lys Lys Cys Tyr Met Met Lys
20 25 30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Lys Phe Ala Leu Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Ile Arg Gln Leu
50 55 60

His Pro Ala Leu Gln Thr Gly Ser Glu Glu Leu Lys Ser Leu Phe Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln
100 105 110

Gln Lys Ile Gln Gln Ala Glu Ala Ala Asp Lys Gly Lys Val Ser Gln
115 120 125

Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala
130 135 140

Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys
145 150 155 160

Ala Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly
165 170 175

Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His
180 185 190

Gln Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala
195 200 205

Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly
210 215 220

Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr

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225                 230                 235                 240

Leu Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val
                245                 250                 255

Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val
            260                 265                 270

Arg Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Lys Gln Gly Pro Lys
        275                 280                 285

Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala
    290                 295                 300

Glu Gln Ser Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu
305                 310                 315                 320

Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly
                325                 330                 335

Pro Gly Ala Ser Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly
            340                 345                 350

Gly Pro Ser His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala
        355                 360                 365

Asn Thr Ser Val Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg
    370                 375                 380

Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn
385                 390                 395                 400


Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
                405                 410                 415

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
            420                 425                 430

Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg
        435                 440                 445

Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr
    450                 455                 460

Thr Pro Gly Gln Lys Gln Glu Ser Lys Asp Arg Glu Thr Leu Thr Ser
465                 470                 475                 480

Leu Lys Ser Leu Phe Gly Asn Asp Pro Leu Ser Gln
                485                 490
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<210> 18
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
signal sequence of HIV strain AF110968

<400> 18
atgcgcgtga tgggcatcct gaagaactac cagcagtggt ggatgtgggg catcctgggc 60
ttctggatgc tgatcatcag c 81

<210> 19
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
signal sequence of HIV strain AF110975

<400> 19
atgcgcgtgc gcggcatcct gcgcagctgg cagcagtggt ggatctgggg catcctgggc 60
ttctggatct gc 72

<210> 20
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
coding sequence of HIV strain AF110965

<400> 20
atgggcgccc gcgccagcat cctgcgcggc ggcaagctgg acgcctggga gcgcatccgc 60
ctgcgccccg gcggcaagaa gtgctacatg atgaagcacc tggtgtgggc cagccgcgag 120
ctggagaagt tcgccctgaa ccccggcctg ctggagacca gcgagggctg caagcagatc 180
atccgccagc tgcaccccgc cctgcagacc ggcagcgagg agctgaagag cctgttcaac 240
accgtggcca ccctgtactg cgtgcacgag aagatcgagg tgcgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag tgccagcaga agatccagca ggccgaggcc 360
gccgacaagg gcaaggtgag ccagaactac cccatcgtgc agaacctgca gggccagatg 420
gtgcaccagg ccatcagccc ccgcaccctg aacgcctggg tgaaggtgat cgaggagaag 480
gccttcagcc ccgaggtgat ccccatgttc accgccctga gcgagggcgc cacccccag 540
gacctgaaca ccatgctgaa caccgtgggc ggccaccagg ccgccatgca gatgctgaag 600
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atcgcccccg gccagatgcg cgagccccgc ggcagcgaca tcgccggcac caccagcacc 720
ctgcaggagc agatcgcctg gatgaccagc aacccccca tccccgtggg cgacatctac 780
aagcgctgga tcatcctggg cctgaacaag atcgtgcgca tgtacagccc cgtgagcatc 840
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cccggcaact tcctgcagag ccgccccgag cccaccgccc cccccgccga gagcttccgc 1380
ttcgaggaga ccacccccgg ccagaagcag gagagcaagg accgcgagac cctgaccagc 1440
ctgaagagcc tgttcggcaa cgacccctg agccagtaa 1479

<210> 21
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
coding sequence of HIV strain AF110967

<400> 21
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ctgcgccccg gcggcaagaa gcactacatg ctgaagcacc tggtgtgggc cagccgcgag 120
ctggagggct tcgccctgaa ccccggcctg ctggagaccg ccgagggctg caagcagatc 180
atgaagcagc tgcagcccgc cctgcagacc ggcaccgagg agctgcgcag cctgtacaac 240
accgtggcca ccctgtactg cgtgcacgcc ggcatcgagg tgcgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag agccagcaga agacccagca ggccaaggag 360
gccgacggca aggtgagcca gaactacccc atcgtgcaga acctgcaggg ccagatggtg 420
caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
ttcagccccg aggtgatccc catgttcacc gccctgagcg agggcgccac cccccaggac 540
ctgaacacca tgctgaacac cgtgggcggc caccaggccg ccatgcagat gctgaaggac 600
accatcaacg aggaggccgc cgagtgggac cgcctgcacc ccgtgcaggc cggccccgtg 660
gccccccggcc agatgcgcga cccccgcggc agcgacatcg ccggcgccac cagcaccctg 720
caggagcaga tcgcctggat gaccagcaac ccccccgtgc ccgtgggcga catctacaag 780
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ctgcgcgccg agcaggccac ccaggacgtg aagaactgga tgaccgagac cctgctggtg 960
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gactgcaccg agcgccaggc caacttcctg ggcaagatct ggcccagcca caagggccgc 1320
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cccgccgaga gcttccgctt cgaggagacc acccccgccc ccaagcagga gcccaaggac 1440
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<210> 22
<211> 502
<212> PRT
<213> Human immunodeficiency virus

<400> 22
Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys
20 25 30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Gly Phe Ala Leu Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ala Glu Gly Cys Lys Gln Ile Met Lys Gln Leu
50 55 60

```
Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Arg Ser Leu Tyr Asn
 65                  70                  75                  80

Thr Val Ala Thr Leu Tyr Cys Val His Ala Gly Ile Glu Val Arg Asp
                 85                  90                  95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Gln
            100                 105                 110

Gln Lys Thr Gln Gln Ala Lys Glu Ala Asp Gly Lys Val Ser Gln Asn
        115                 120                 125

Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile
    130                 135                 140

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala
145                 150                 155                 160

Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala
                165                 170                 175

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
            180                 185                 190

Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu
        195                 200                 205

Trp Asp Arg Leu His Pro Val Gln Ala Gly Pro Val Ala Pro Gly Gln
    210                 215                 220

Met Arg Asp Pro Arg Gly Ser Asp Ile Ala Gly Ala Thr Ser Thr Leu
225                 230                 235                 240

Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Val Pro Val Gly
                245                 250                 255

Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
            260                 265                 270

Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
        275                 280                 285

Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu
    290                 295                 300

Gln Ala Thr Gln Asp Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
305                 310                 315                 320

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro
                325                 330                 335

Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
            340                 345                 350

Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala Asn
        355                 360                 365
```

```
Ser Val Asn Ile Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg
    370                 375                 380

Asn Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Lys Asn
385                 390                 395                 400

Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
                405                 410                 415

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
            420                 425                 430

Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg
        435                 440                 445

Ser Glu Pro Ala Ala Pro Thr Val Pro Thr Ala Pro Pro Ala Glu Ser
    450                 455                 460

Phe Arg Phe Glu Glu Thr Thr Pro Ala Pro Lys Gln Glu Pro Lys Asp
465                 470                 475                 480

Arg Glu Pro Tyr Arg Glu Pro Leu Thr Ala Leu Arg Ser Leu Phe Gly
                485                 490                 495


Ser Gly Pro Leu Ser Gln
            500


<210> 23
<211> 849
<212> PRT
<213> Human immunodeficiency virus

<400> 23
Met Arg Val Met Gly Ile Leu Lys Asn Tyr Gln Gln Trp Trp Met Trp
  1               5                  10                  15

Gly Ile Leu Gly Phe Trp Met Leu Ile Ile Ser Ser Val Val Gly Asn
             20                  25                  30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Lys
         35                  40                  45

Thr Thr Leu Phe Cys Thr Ser Asp Ala Lys Ala Tyr Glu Thr Glu Val
     50                  55                  60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65                  70                  75                  80

Gln Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
                 85                  90                  95

Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
            100                 105                 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
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        115                 120                 125

Lys Cys Arg Asn Val Asn Ala Thr Asn Asn Ile Asn Ser Met Ile Asp
    130                 135                 140

Asn Ser Asn Lys Gly Glu Met Lys Asn Cys Ser Phe Asn Val Thr Thr
145                 150                 155                 160

Glu Leu Arg Asp Arg Lys Gln Glu Val His Ala Leu Phe Tyr Arg Leu
                165                 170                 175

Asp Val Val Pro Leu Gln Gly Asn Asn Ser Asn Glu Tyr Arg Leu Ile
            180                 185                 190

Asn Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe
        195                 200                 205

Asp Pro Ile Pro Ile His Tyr Cys Thr Pro Ala Gly Tyr Ala Ile Leu
    210                 215                 220

Lys Cys Asn Asn Gln Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val
225                 230                 235                 240

Ser Ser Val Gln Cys Ala His Gly Ile Lys Pro Val Val Ser Thr Gln
                245                 250                 255

Leu Leu Leu Asn Gly Ser Leu Ala Lys Gly Glu Ile Ile Ile Arg Ser
            260                 265                 270

Glu Asn Leu Ala Asn Asn Ala Lys Ile Ile Ile Val Gln Leu Asn Lys
        275                 280                 285

Pro Val Lys Ile Val Cys Val Arg Pro Asn Asn Asn Thr Arg Lys Ser
    290                 295                 300

Val Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile
305                 310                 315                 320

Gly Asp Ile Arg Gln Ala Tyr Cys Ile Ile Asn Lys Thr Glu Trp Asn
                325                 330                 335

Ser Thr Leu Gln Gly Val Ser Lys Lys Leu Glu Glu His Phe Ser Lys
            340                 345                 350

Lys Ala Ile Lys Phe Glu Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr
        355                 360                 365

Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asp Thr Ser
    370                 375                 380

Gln Leu Phe Asn Ser Thr Tyr Ser Pro Ser Phe Asn Gly Thr Glu Asn
385                 390                 395                 400

Lys Leu Asn Gly Thr Ile Thr Ile Thr Cys Arg Ile Lys Gln Ile Ile
                405                 410                 415

Asn Met Trp Gln Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala
```

```
            420                 425                 430

Gly Asn Leu Thr Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg
        435                 440                 445

Asp Gly Gly Lys Thr Gly Pro Asn Asp Thr Glu Ile Phe Arg Pro Gly
    450                 455                 460

Gly Gly Asp Met Arg Asp Asn Trp Arg Asn Glu Leu Tyr Lys Tyr Lys
465                 470                 475                 480

Val Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg
                485                 490                 495

Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val Phe
            500                 505                 510

Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Ile
        515                 520                 525


Thr Leu Thr Val Gln Ala Arg Leu Leu Leu Ser Gly Ile Val Gln Gln
    530                 535                 540

Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln
545                 550                 555                 560

Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg Ile Leu Ala Val
                565                 570                 575

Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser
            580                 585                 590

Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ser Ser Trp Ser
        595                 600                 605

Asn Arg Ser His Asp Glu Ile Trp Asp Asn Met Thr Trp Met Gln Trp
    610                 615                 620

Asp Arg Glu Ile Asn Asn Tyr Thr Asp Thr Ile Tyr Arg Leu Leu Glu
625                 630                 635                 640

Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu
                645                 650                 655

Asp Ser Trp Gln Asn Leu Trp Asn Trp Phe Ser Ile Thr Asn Trp Leu
            660                 665                 670

Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu
        675                 680                 685

Arg Ile Ile Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly
    690                 695                 700

Tyr Ser Pro Leu Pro Phe Gln Thr Leu Thr Pro Asn Pro Arg Glu Pro
705                 710                 715                 720
```

```
Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Gly
                725                 730                 735

Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu Ala Trp Asp Asp
            740                 745                 750

Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Phe Ile
        755                 760                 765

Leu Ile Ala Ala Arg Val Leu Glu Leu Leu Gly Gln Arg Gly Trp Glu
    770                 775                 780

Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu
785                 790                 795                 800

Lys Lys Ser Ala Ile Ser Leu Leu Asp Thr Ile Ala Ile Ala Val Ala
                805                 810                 815


Glu Gly Thr Asp Arg Ile Ile Glu Phe Ile Gln Arg Ile Cys Arg Ala
            820                 825                 830

Ile Arg Asn Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu
        835                 840                 845

Gln
```

<210> 24
<211> 855
<212> PRT
<213> Human immunodeficiency virus

<400> 24

```
Met Arg Val Arg Gly Ile Leu Arg Ser Trp Gln Gln Trp Trp Ile Trp
  1               5                  10                  15

Gly Ile Leu Gly Phe Trp Ile Cys Ser Gly Leu Gly Asn Leu Trp Val
             20                  25                  30

Thr Val Tyr Asp Gly Val Pro Val Trp Arg Glu Ala Ser Thr Thr Leu
         35                  40                  45

Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val His Asn Val
     50                  55                  60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile
 65                  70                  75                  80

Glu Leu Asp Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met
                 85                  90                  95

Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
            100                 105                 110

Lys Pro Arg Val Lys Leu Thr Pro Leu Cys Val Thr Leu Lys Cys Thr
```

```
        115                 120                 125

Asn Tyr Ser Thr Asn Tyr Ser Asn Thr Met Asn Ala Thr Ser Tyr Asn
    130                 135                 140

Asn Asn Thr Thr Glu Glu Ile Lys Asn Cys Thr Phe Asn Met Thr Thr
145                 150                 155                 160

Glu Leu Arg Asp Lys Lys Gln Gln Val Tyr Ala Leu Phe Tyr Lys Leu
                165                 170                 175

Asp Ile Val Pro Leu Asn Ser Asn Ser Ser Glu Tyr Arg Leu Ile Asn
            180                 185                 190

Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp
        195                 200                 205

Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys
    210                 215                 220

Cys Lys Asn Asn Thr Ser Asn Gly Thr Gly Pro Cys Gln Asn Val Ser
225                 230                 235                 240

Thr Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Pro Leu
                245                 250                 255

Leu Leu Asn Gly Ser Leu Ala Glu Gly Gly Glu Ile Ile Ile Arg Ser
            260                 265                 270

Lys Asn Leu Ser Asn Asn Ala Tyr Thr Ile Ile Val His Leu Asn Asp
        275                 280                 285

Ser Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly
    290                 295                 300

Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Glu Asn Ile Ile
305                 310                 315                 320

Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Ala Gly Glu Trp Asn
                325                 330                 335

Lys Ala Val Gln Arg Val Ser Ala Lys Leu Arg Glu His Phe Pro Asn
            340                 345                 350

Lys Thr Ile Glu Phe Gln Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr
        355                 360                 365

Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Ser
    370                 375                 380

Lys Leu Phe Asn Ser Ser Tyr Asn Gly Thr Ser Tyr Arg Gly Thr Glu
385                 390                 395                 400

Ser Asn Ser Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile
                405                 410                 415

Asp Met Trp Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu
```

```
            420                 425                 430

Gly Asn Ile Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg
        435                 440                 445

Asp Gly Gly Leu Asp Asn Ile Thr Thr Glu Ile Phe Arg Pro Gln Gly
    450                 455                 460

Gly Asp Met Lys Asp Asn Trp Arg Asn Glu Leu Tyr Lys Tyr Lys Val
465                 470                 475                 480

Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg Arg
                485                 490                 495


Val Val Glu Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val Ile Phe
            500                 505                 510

Gly Phe Leu Gly Ala Ala Gly Ser Asn Met Gly Ala Ala Ser Ile Thr
        515                 520                 525

Leu Thr Ala Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln
    530                 535                 540

Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Met Leu Gln Leu
545                 550                 555                 560

Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Ile Glu
                565                 570                 575

Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
            580                 585                 590

Lys Leu Ile Cys Thr Thr Thr Val Pro Trp Asn Ser Ser Trp Ser Asn
        595                 600                 605

Lys Thr Gln Gly Glu Ile Trp Glu Asn Met Thr Trp Met Gln Trp Asp
    610                 615                 620

Lys Glu Ile Ser Asn Tyr Thr Gly Ile Ile Tyr Arg Leu Leu Glu Glu
625                 630                 635                 640

Ser Gln Asn Gln Gln Glu Gln Asn Glu Lys Asp Leu Leu Ala Leu Asp
                645                 650                 655

Ser Arg Asn Asn Leu Trp Ser Trp Phe Asn Ile Ser Asn Trp Leu Trp
            660                 665                 670

Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg
        675                 680                 685

Ile Ile Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr
    690                 695                 700

Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Asn Pro Arg Gly Leu Asp
705                 710                 715                 720
```

```
Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Asp Arg
                725                 730                 735

Ser Ile Arg Leu Val Gln Gly Phe Leu Ala Leu Ala Trp Asp Asp Leu
            740                 745                 750

Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Ile Leu
        755                 760                 765

Val Thr Ala Arg Val Val Glu Leu Leu Gly Arg Ser Ser Pro Arg Gly
    770                 775                 780


Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln
785                 790                 795                 800

Tyr Trp Gly Leu Glu Leu Lys Lys Ser Ala Thr Ser Leu Leu Asp Ser
                805                 810                 815

Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Ile Ile Glu Val Ile
            820                 825                 830

Gln Arg Ile Tyr Arg Ala Phe Cys Asn Ile Pro Arg Arg Val Arg Gln
        835                 840                 845

Gly Phe Glu Ala Ala Leu Gln
    850                 855


<210> 25
<211> 20
<212> PRT
<213> Human immunodeficiency virus

<400> 25
Asp Ile Lys Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
  1               5                  10                  15

Phe Phe Lys Thr
             20


<210> 26
<211> 60
<212> DNA
<213> Human immunodeficiency virus

<400> 26
gacataaaac aaggaccaaa agagcccttt agagactatg tagaccggtt ctttaaaacc 60

<210> 27
<211> 20
<212> PRT
<213> Human immunodeficiency virus

<400> 27
Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
```

```
  1               5                  10                  15

Phe Phe Lys Thr
             20
```

<210> 28
<211> 47
<212> PRT
<213> Human immunodeficiency virus

<400> 28

```
Thr Ile Thr Ile Thr Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln
  1               5                  10                  15

Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Leu Thr
             20                  25                  30

Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
         35                  40                  45
```

<210> 29
<211> 48
<212> PRT
<213> Human immunodeficiency virus

<400> 29

```
Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asp Met Trp
  1               5                  10                  15

Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu Gly Asn Ile
             20                  25                  30

Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg Asp Gly Gly
         35                  40                  45
```

<210> 30
<211> 4
<212> PRT
<213> Human immunodeficiency virus

<400> 30

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Gly Gly Gly Ser
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